```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 14, 2001, 16:12:19 ; Search tlme 21.02 Seconds
(without alignments)
1466.551 Million cell updates/sec

US-09-455-486-6 2351 Title: Perfect score:

1 MESISMMGSPKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454 sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

195891 seqs, 67900655 residues Searched:

195891 Total number of hlts satisfying chosen parameters:

Minimum DB seq Maximum DB seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:*
1: pirl:*
2: pir2:*
3: plr3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	o Ouery Match Length	DB	ID	Description
-	156.5	6.7	239	7	T50571	probable oxidoredu
7	147	6.3	213		H69400	conserved hypothet
m	142	9.0	212	7	D69361	
4	142	0.9	224		T10120	F420-dependent NAD
S	133	5.7	223	7	D64487	hypothetical prote
9	120.5	5.1	232	ď	A69131	conserved hypothet
7	119.5	5.1	216	7	T00121	hypothetical prote
œ	116.5	5.0	242	7	G82642	conserved hypothet
on.	111.5	4.7	695	7	JN0896	follitropin_recept
10	111.5	4.7	1228	~	S59681	probable membrane
11	110.5	4.7	694	~	JC4301 .	foll1tropin recept
12	109	4.6	320	7	T28379	ORF MSV218 hypothe
13	109	4.6	712	7	820969	probable membrane
14	109	4.6	1184	7	H71436	hypothetical prote
	107.5	4.6		~ 1	S60385	probable membrane
16	107.5	4.6		-	.QRHUFT	follitropin recept
17	105	4.5	442	7	B64582	sodlum- and chlori
18	105	4.5	604	(7	T31042	hypothetical prote
19	. 104	4.4	396	-	C64907	chloramphenicol re
20	103	4.4	465	~	S69915	sodium-phosphate t
21	102.5	4.4	1242	~	T39453	probable mrna stab
22	102	4.3		~	T41068	hypotheticai prote
23	101	4.3		7	E71139	hypothetical prote
24	101	4.3	348	7	T12284	NADH dehydrogenase
25.	101	4.3	420	7	F69144	O-antigen transpor
, 26	101	4.3	501	7	T02134	hypothetical prote
27	101	4.3	735	7	A83006	hypothetical prote
28	100.5	4.3	346	7	_	6
29	100	4.3	395	7	C71219	hypothetical prote

endonuclease Scel	NADH dehydrogenase	NADH dehydrogenase	NADH dehydrogenase	probable transport	hypothetical prote	genome polyprotein	genome polyprotein	hypothetical prote	follicle stimulati	NADH dehydrogenase	NADH dehydrogenase	follitropin recept	polycystic kidney	ferric reductase (hypothetical prote
A28439	C71391	112290	T12281	G71930	T05845	GNWVY	GNWVYP	A70417	I45896	T11325	T12283	A34548	G02640	S30075	T25281
7	7	N	7	7	7	Т	7	7	7	7	.7	7	ď	7	7
476	452	348	348	442	962	3411	3411	268	695	346	348	692	809	989	711
4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.	4.1	4.1	4.1	4.1	4.i	4.1	4.1
100	99.5	96	96	98	98	98	86	97.5	97.5	26	26	45	96.5	96.5	96.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

probable oxidoreductase [imported] - Streptomyces coelloclor C;Species: Streptomyces coelloclor C;Date: 21-Jul-2000 *sequence_revision 21-Jul-2000 *text_change 28-Jul-2000

C;Accession: T50571
R;Redenbach, M.; Kieser, H.M.: Denapaite, D.; Elchner, A.; Cullum, J.; Kinashi, H.; H.Mol. Microbiol. 21, 77-96, 1996
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 M. A;Reference number: 220556; Muin:97000351
A;Reference num

A; Molecule type: DNA A; Residues: 1-239 <RED>

A;Cross-references: EMBL:AL133220; PIDN:CAB61708.1 A;Experimental source: strain A3(2)

C.Genetics: A.Note: SCC75A.08c C.Superfamily: conserved hypothetical protein MJ1501

10: Gaps 25 IKDARKVTVGVI-GSGDFAKSLTIRLIRCGYHVVIGSR---NPKFASEFFPHYVDVTHHE 80 6.7%; Score 156.5; DB 2; Length 239; 27.9%; Pred. No. 3.5e-05; Live 41; Mismatches 72; Indels 45. Query Match Best Local Similarity 27.99 Matches 61; Conservative õ

81 DALIKTNIIFVAIHRE-HYTSLWDLRHLLVGKILIDVSNNMRINQ-----YPE--SNAE 131 ò

8

٠.

83 g 132 YLASLFPDSLIVKGFNVVSAWALQ-------LGPKDASRQVYICSNNIQARQQV 178 g ò

179 IELARQLNFIP----IDLGSLSSAREIENLPLRLFTLWR 213 ŏ

-- LAGR---IPGMRGVFAGRLRNAHQVESLVANLISVNR 226 193 Q

RESULT H69400

conserved hypothetical protein AF1209 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Catec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: H69400
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
F;Elelschmain, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gili, S.: Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

16:24:14

14

Wed Mar

us-09-455-486-6.rpr

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Cyaccession: D64487
R/BULL, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R/BULL, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R/BULL, C.J.; White, O.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrikk, J.M.; Glodek, rson, J.D.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. A;Authors: Kalne, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999
A;Accession: D64487
A;Stetus: Preliminary, nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                            F420-dependent NADP reductase (EC 1.6.8.-) - Methanobacterium thermoautotrophicum (st C; Species: Methanobacterium thermoautotrophicum (c; Species: Methanobacterium thermoautotrophicum (c; Date: 16-Jul-1999 #text_change 20-Jun-2000 C: Accession: 110120 R: Berk, H.; Thauer, R.K. FEBS Lett. 438, 124-126, 1998 A; Title: F420H2:NADP oxidoreductase from Methanobacterium thermoautotrophicum: identi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U67591; GB:L77117; NID:92826422; PIDN:AAB99514.1: PID:91500389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVAILTVPLQAQMAT-LGSVKEAIKGKVLIDATVPIDSCLGGSAVRYIDLMDGSAAERAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLFPD--SLIVKGFNVVSAWALQ--LGPKDASRQVYICSNNIQARQQVIELARQLNFI-P 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GTGDQGLGLALRLALAGEEVIIGSRDAEKAVSAAQKVLEIAERDDLKVKGATNAEAAEEA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 GSGDFAKSLIIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTK--TN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 133; DB 2; Le
21.9%; Pred. No. 0.0024;
"International 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Stolecule type: DNA
A.Residues: 1-224 <BER>
A.Cross-references: EMBL:Y17210
A.Experimental source: strain Marburg
C.Superfamily: conserved hypothetical protein MJ1501
C.Steywords: Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
6.0%; Score 142; DB 2;
Best Local Similarity 29,2%; Pred. No. 0.00046;
Matches 59; Conservative '29; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: REVI473617-1472946
C;Superfamily: conserved hypothetical protein MJ1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A: Reference number: 216959; MUID:99037734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | | :|| || :|| || 185 IDCGGLENARVIEKITPLLINL 206
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                  188 VESLTPLILNIMR 200
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hes 46; Conserve
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D69361
conserved hypothetical protein AF0892 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: D69361
R;Klenk, H.D.; Ober-Levision 05-Dec-1997 *text_change 29-Sep-1999
C;Accession: D69361
R;Klenk, H.D.; Clayton, R.J.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
S;Klenk, H.D.; Clayton, R.D.; Cocayne, J.D.; Weldman, J.F.; McDonald, E.
Natures 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.: Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.: Venter, J.C.
A,Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250: MUID:98049343
A,Accession: H69400
A,Status: prellminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-213 < KLE>
A,Cross-references: GB:AE001021; GB:AE000782; NID:92689344; PIDN:AAB90038.1; PID:9264937
C;Superfamily: conserved hypothetical protein MJ1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-212 <KLE>
A;Cross-references: GB:AEOO1042; GB:AEO00782: NID:g2689365; PIDN:AAB90348.1; PID:g264976
C;Superfamily: conserved hypothetical protein MJ1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local Similarity 27.5%
Matches 56; Conservative
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                                                                                                           Query Match
Best Local Similarity 23.7%
Conservative
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Matches 46; Conservative
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A, Residues: 1-242 <SIM>
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A;Status: preliminary
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C;Species: Leptospira interrogans
C;Species: Leptospira interrogans
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000'
C;Accession: T00121
R;Takahashi, Y.; Akase, K.; Hirano, H.; Fukunaga, M.
Gene 215, 37-45, 1998
A;Title: Physical and genetic maps of the Leptospira Interrogans serovar icterohaemorrha
                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein MTH248 - Methanobacterium thermoautotrophicum (strain Del Cispecias: Methanobacterium thermoautotrophicum
C;Specias: Methanobacterium thermoautotrophicum
C;Declas: Methanobacterium thermoautotrophicum
C;Declas: Methanobacterium thermoautotrophicum
C;Accession: A69131
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; (Alu, D.; Spadafora, R.; Vacalre, R.; Wang, Y.; Wherzbowski, J.; Gibson, R.; Jiwani, N.; Alu, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeiling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514
A:Accession: A69131
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A;Experimental source: strain Delta H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABERAARFLREQGTRVAAAFNNISASALLEVSEPVDCDCLVASDHRDALEVAAELAEKID 186
                                                                                                                                                    130 AEYLASLF---PDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186
                                                                    134 ASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQOVIELARQLNFI-PIDL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DALTKTNIIFVAIH-REHYTSLWDLRHLLVGKILIDVS------NNMRINQYPESN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDAAASADVVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGDQGFGLALRLAK-NNKIIIGSRKKEKAEEAAKKAKEILKQRGIEADIIGLENKDAAK
                                         KTNIIFVAIHREH-YTSLWDLRHLLVGKILIDV------SNNMRINQYPE-SNAEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 KVTVGVIGSGDFAKSLIIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 120.5; DB 2;
23.8%; Pred. No. 0.024:
tlve 42; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Start codon: TTG
C;Superfamily: conserved hypothetical proteln MJ1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T00121
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                  193 GSLSSAREIENLPLRLFTLWRGPVVVAISL 222
                                                                                                                                                                                                                                                           187 GNLEKSRITEAIT------PLLIGLNI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 214115; MUID: 98332717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 FI-PIDLGSLSSAREIENLPLRLFTL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.8%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-232 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: MTH248
                                                                                  29
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Ristmental Source: strain 95C
Ristmental Source: Strain Source: Submitted to GenBank, June 2000
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Ristment Source: Submitted to GenBank, June 2000
Ristment Source: Submitted to GenBank, June 2000
Ristment Source: Submitted Source: Submitted to GenBank, June 2000
Ristment Source: Remer, Remer, Remer, Remer, Remer, Remer, Randence, M.C.; Franco, M.C.; Franco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein XP1737 [imported] - Xylella fastidiosa (strain 9a5c) C; Species: Xylella fastidiosa (c) atea 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: GB2542 (S) Aug-2000 #sequence_revision Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
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A;Molecule type: DNA
A;Residues: 1.216 cmpc
A;Cross-references: EMBL:AB010203; NID:g2780763; PIDN:BAA24368.1; PID:g2780765
A;Experimental source: strain Ictero No.1; substrain icterobaemorrhagiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 TKINIIFVAIHREHYTSLW-DLRHLLVGKILIDVSNNMRINQ---YPESN----AEYLAS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 EFGTVLLLAVPFEALPQVGRDLRSAYRGKIVLDSTNPWGASSADVYREARELGVAQTVVK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---INOYPESNAEYLASL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPDSLIVKGFNVVSAWALQLGP--KDASRQVYICSNNIQARQQVIELARQLNFIFIDLGS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ARKVIVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNP----KFASEFFPHVVDVTHHEDAL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 VGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHV---VDVTHHEDALIKTNII 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: AB2515; MUID:20365717
A,Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 AAPMRIGVIGAGSLGGIVGRLWVKAGHEVMFSSRNPDKLEAMARELEPR-ASVGQPLAAT
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                                                                                                                                                                                                                                                                                                                                                                Length 216:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
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                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 119.5; DB 2; 23.7%; Pred. No. 0.026;
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14.0%; Pred. No. 0.053;
ve. 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
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OV 136 LFPDSLIVKGFNVVSAWALOLGPKDASROVYICSNNIOAROOVIELAROLNFIPI 190	OV 307ILSEPPAMVHVAVSICT.DMBRGERVIET.NMAVOOVHANTENS 246
: : : :	362 YNILRVLIWFISILAITGNIIVLVTLTTSQYKLTVPRFLMCNLAFAD
Qy 191 DLGSLSSAREIE 202	Qy 349 WNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLG 399
: 5	Db 409
RECALL 4	OY 400YVALLISTEHVLIYGWKRAFEEEXYRFYTPPNFV-LAL 436
9580NL	Db 457 VYTLTAITLERWHTITHAMQLDCKVHVRHAASVWVWGWIFAFAAALFPIFGISSYWKVSI 516
Noticenter names: follicle-stimutating hormone receptor (FSHR)	Qy 437 VLPSIVILDILQL 449
C. process. marces tasciculairs (crap-earing marcaque) C. bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C. accession: .mon948. s.s.d.s.	Db 517 CLPMDIDSPLSQL 529
	RESULT 10
A;Title: Molecular cloning of the testicular follicle stimulating hormone receptor of the A;Reference number: JNO898; MUID:94071854	S59681 probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
A;Accession: JN0898 A;Molecule type: mRNA	N.Alternate names: hypothetical protein LPA5w; hypothetical protein YP8132.01 C.Species: Saccharomyces cerevisiae
A:Residues: 1-695 <gro> A:Cross·references: EMBL:X74454; NID:g396801; PIDN:CAA52463.1; PID:g396802</gro>	996 #text_change 12-Dec
A;Note: the authors translated the codon AGT for residue 488 as Arg C;Function:	
A; Description: receptor that mediates the biochemical effects of follitropin C; Superfamily: glycoprotein hormone receptor; leucine-rich aipha-2-glycoprotein repeat }	
C:Keywords: G protein-coupled receptor; glycoprotein: hormone receptor; phosphoprotein; F:1-17/Domain: signal sequence #status predicted <sig></sig>	
F:18-695/Product: follitropin receptor #status predicted <pfh></pfh>	
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr3></lrr3>	
F;121-145/Domain: Leucine-rich alpha-2-glycoproteln repeat homology <lrr4> . F;146-169/Domain: ieucine-rich alpha-2-glycoprotein repeat homology <lrr5></lrr5></lrr4>	
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr6> F;194-216/Domain: leucine-rich alpha-2-glycoprotein repeat homology <lrr7></lrr7></lrr6>	
F;367-387/Domain: transmembrane #status predicted <tm1> F;399-421/Domain: transmembrane #status predicted <tm2></tm2></tm1>	
F:444-465/Domain: transmembrane #status predicted <tm3> F:486-508/Domain: transmembrane #status predicted <tm4> '.</tm4></tm3>	
F:529-550/Domain: transmembrane #status predicted <tm5> F:574-597/Domain: transmembrane #status predicted <tm6></tm6></tm5>	
F:609-630/Domain: transmembrane #status predicted <tm7> F:191.199,293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted</tm7>	F;125-141/Domain: transmen F;478-494/Domain: transmen
F:555/Hinding Site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F:556/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted	rane #status predicted
Ouery Match 4.7%: Score 111.5: DB 1: Length 695:	Query Match 4.7%; Score 111.5; DB 2; Length 1228; Rest Local Similarity 19 0%: pred No 1:
Best Local Similarity 17.0%; Pred. No. 0.5; Matches 84; Conservative 75; Mismatches 151; Indels 183; Gaps 16;	Conservative 71; Mis
121	
Db 98 HEIRIEKANNL-LYINPEAFQNLPNLRYLLISNTGIKHLPDVHKIHSFQKVLLDIQDNIN 156	Db 292 KTMAETTISSGLAENKYLRVLDTIFALKPSNVDTLLTKSWIAVVIKGMSTYATHQPLKAL 351
QY 122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181	51 RCGYHVVIGSRNPKFASEFFPHVVDVTHHEDAL
Db 157 IH1IERNSFVGLSFESVILWLNKNGIQEIHNCA189	352 RKIPGVFHINCTYLASETPEVYQAASQCLISILSESVKDDLLLYTPSVDEKVFKNVD
QY 182 ARQLNFIPIDLGSLSSAREIENLPLREFTLARGPVVVALSLATFFFLYSFVRDVIHPYAR 241	OY 64TRINIEWITHREHYTSLWDIRHLIVGKILIDVSNNWRINOYPESNAEYLASLF 137 Dh 409 ETISOTAWTRIDE/GIRVSHGSPRTIFITI.AABNKPRYBRUDHEIRS: 466
Db 190FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246	TOTAL THE TAXABLE STATES OF THE STATES OF TH
Qy 242 NQSSEYRIPIEIVNKTLPIVAITLELSLVY	QY ISO FUSITIVES OF VERIFY CANDELS OF THE SURTED TO THE SU
SLEK	189PIDIGSLSSARETENLDLRIETARGDVVVAISLAFFELVSEVENUT
QY 272	489 PEMILAEAPLALDAPSSERPGRAMLLPLIRDYTKNANLATFQNEL
302 DIMINITALEGENSSINGSTONES DMITHER DIDDONES VOVICE PREDIGN	

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A; Cross-references: EMBL: AF063866; NID: 94049647; PIDN: AAC97747.1; PID: 94049787
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5. Affonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. J. Virol. 73, 533-552, 1999
A; Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A; Reference number: 220484; MUID: 99102612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 VVDVTHHEDALTKTNIIFV------AIHREHYTSLWDLRHLLVGKILIDVSNN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ILKNIFPK------LUSNELSIYIYNNELSKYINHIEVLYREYYTKLF------LUSNELDENHN 111
                                                                                                                                                                                                                                                                                                                                                                                                                400 YVALLISTFH-------VLIYGWKRAFEEEYYRFYTPPNFV-LALVLP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : || : :|| : ::| | : 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164. QVY1-------CSNNIQARQQVIELARQLNFIPIDLGSLSSAREI--ENLPL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 RLFILWRGPVV-----VAISLATFFFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 ALYIMYKSKKILKYNKYKLLKILFPNTYDEYYFKNDII--YNSNEYYDFHNFDIYNAIKT 282
     ----FNGTQLDELNLSDNDNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKL 243
                                                                                         244 RARSTYNLKKLPTLEKFVTLMEASLTYPSHCCAFANWRRQISDLHPICNKSILRQEVDVM 303
                                                                                                                                                              S----LVYLAGLLAAAYQLYYGTKYRRF-------PPWLETWLQCRKQLG---306
                                                                                                                                                                                                                304 TOARGORVSLAEDGESSLAKEFDTMYSEFNYDLCNEVVDVICSPKPDAFNPCEDIMGHDI 363
                                                                                                                                                                                                                                                                        ----YSLCLPMRRSERYLFLNMAYQQVHANIENSWNE 351
                                                                                                                                                                                                                                                                                                                             --- 407
                                                                                                                                                                                                                                                                                                                                                                            352 EEVWRIEMYISFGIMSLCLLSLLAVTSIPSVSNALNWRE-----FSFIQSTLG--- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 TC---LPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPH 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 TCSQVINNPLYNIKDSKKVCI-----IHKNYYKKILCENYHLENKSRNIK---KYFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 MRINOYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASR------
                                                                                                                                                                                                                                                                                                      Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 109; DB
; Pred. No. 0.3;
63; Mismatches
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                                                       240 ARNQOSDFYKIPI-----
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Best Local Similarity 19.3%
Matches 58; Conservative
                                                                                                                                                                                                                                                                        --LLSFFFAMVHVA----
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A;Title: The porcine follitropin receptor: CDNA cloning, functional expressionand chromd A;Reference number: JC4301; MDID:96011644
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A;Gene: fahr
A;Gene: fahr
A;Gene: fahr
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A;Gene: fahr
C;Genetics:
C;Genetics:
C;Generics:
C;Generics:
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat b
C;Superfamily: glycoprotein hormone binding #status predicted +HOB>
C;Reywords: G protein-coupled receptor; hormone binding #status predicted +HOB>
E;1-365/Domain: follicle-stimulating hormone binding #status predicted +HOB>
E;366-388/Domain: transmembrane #status predicted <TM2>
E;366-388/Domain: transmembrane #status predicted <TM3>
E;443-464/Domain: transmembrane #status predicted <TM4>
E;528-549/Domain: transmembrane #status predicted <TM5>
E;528-549/Domain: transmembrane #status predicted <TM5>
E;608-629/Domain: transmembrane #status predicted <TM5>
E;608-629/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC4301
A; Molecule type: mRNA
A; Residues: 1-694 ARBWA
A; Cross-references: GB:L131966
A; Experimental source: ovarian granulosa cells
C: Comment: This receptor belongs to the family of the G-protein coupled receptors. It
ermatogenesis in male and oogenesis in female.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             follitropin receptor - pig
NyAlternate names: follicle-stimulating hormone receptor
NyAlternate names: follicle-stimulating hormone receptor
C;Species: Sus Scrofa domestica (domestic pig)
C;Species: Sus Scrofa domestica (domestic pig)
C;Species: J6-Nov-1995 #sequence_revision O8-Feb-1996 #text_change 21-Jan-2000
C;Accession: J64301
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                                                                                                         303
                                                                                                                                                                                                             304 QLGLLSFFFAMVHVAYSLCLPMRRS-----ERYL-----FLNMAYQQVHANIENSWNE 351
                                                                                                                                                                                                                                                  STALLAVLENV ----YTQTTPNARSYILETIDQYLKITSKEDLEKTENNVCGLLKNSMNE 704
                                                                                                                                                                                                                                                                                                                       EEVWRIEMYISFGIMSLGLLSLL--AVTSIPSVSNALNWREFSFIQSTLGYVALLISTFH 409
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  -IVAITLLSL 269
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                                               534 APYIKSFÖSKFDKVPEESIQLRVFQTIVDQIWSTLPRFCELPMDLRESFTDEFASELSSL
                                                                                                                                                         594 LYSEVELRTTICHALKVLAESNVSYAEESSSHNVLLLQRFPISEAQKNIEYLST----K
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16.5%; Pred. No. 0.6;
iive 90; Mismatches 170;
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hypothetical protein - Arabidopsis thaliana
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                                                                                        probable membrane protein YLL051c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L0593
C;Species Saccharomyces cerevisiae
C;Dete: 11-Feb-1995 #sequence_revision 12-May-1995 #text_change 20-Jun-2000
C;Accession: S50969: S64803
E;Wedler, H.;Wambutt, R.
submitted to the EMBL Data Library, January 1995
A;Bescription: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 PPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLS 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 H-VAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-712 <WEW>
A;Cross-references: EMBL:273156; NIQ:91360252: PID:91360253; MIPS:YLL051c
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 4.6%; Score 109; DB 2; Length 712; Best Local Similarity 18.8%; Pred. No. 0.82; Matches 72; Conservative 51; Mismatches 119; Indeis 142;
                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:247973; NID:g642313; PID:g642333 R;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R. submitted to the Protein Sequence Database, May 1996;
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CTM3>
CTM4>
CTM5>
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P:172-18B/Domain: transmembrane #status predicted
P:245-261/Domain: transmembrane #status predicted
P:245-203/Domain: transmembrane #status predicted
P:364-380/Domain: transmembrane #status predicted
P:364-380/Domain: transmembrane #status predicted
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A;Cross-references: SGD:S0003974; MIPS:YLL051c
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C; Superfamily: ferric reductase FRE2
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239 MPNSL----EAW----
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A;Accession: S64803
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A; Residues: 1-712 <WED>
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RESULT H71436

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C.; Chaiwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t A;Reference number: A71400; MUID:98121113
A;Reference number: A71436
                                                                                                                                                                        R.Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D. P.; Wedler, H.; Wedler, E.: Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn., N.; G. avanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.O.; Rieger, M.; Schaeffer, M.; Funk, B. A.; Auture 31, 485-488, 1998
A.; Authors: Mueller-Auer, S.: Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdomen erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Saccharomyces cerevisiae
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
C;Accession: S60385; S66849; S57673
R:Casamayor, A.; Aldea, M.; Casas, C.; Herrero, E.; Gamo, F.J.; Lafuente, M.J.; Gance Yeast 11, 1281-1288, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1184 <BEV> A;Cross-references: GB:297342; NID:92245031: PIQ:e327022
C.Species: Arabidopsis thallana (mouse-ear cress)
A:Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    654 SSIQNATKLIYLDMSDCKKLESFPTDLNLESLEYLNLTGCPNLRNFPAIKMGCSDVDFPE 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 NPKFASEFFPHYVDVTHHEDALTKT---NIIFVAIHREHYTSLWDLRHLLVGKILIDVSN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 GMRNLQYLEIGYYGDLPOSLVYLPLKLRLLDWDDCPLKSLPSTFKAEYLV----NLIMK 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SLSSAREIENLP--LRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 WLQCRKQLGLLSFFFAMVHVAYSLCLPMR-RSERYLFLNMAYQQVHANIENSWNEEEVWR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               768 -----GIOSLGSLEGMDLSESENLTEIPDLSKATKLESLILNNCKSLVTLPSTIGNLH 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probabie membrane protein YQL152w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein AQB629; hypothetical protein 00443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NAEYLASLFPDSLIVK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 ARNQOSDFYKIPIE--IVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLET 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          735 YLDC------RGYKHEKLWE 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 IEMYISFGIMSLGLLSLL-----AVTSIPSVSNAL------NWREFSFIQSTLGYVA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 CLPNG--INGIKDARKVTVGVIGSGDFAKSLTIRLIRCGY---HVVI------GSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 GNPGKRRFLTNFEDI -- HEVVTEKTGTETLLGIRLPFEEYFS---TRPLLIDK---ESFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 GFNVVSAW--ALQLGPKDASRQVYICSNNIQARQQVIBLARQLNFIPIDLG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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4.6%; Score 109: DB 2; L
Best Local Similarity 21.7%; Pred. No. 1.6;
Matches 105; Conservative 55; Mismatches 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 NMRINOY------PES------
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Arithe: DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome Areference number: $60385; MUD: 96132030
Arecession: $60385
Arecession: $60385
Arecession: $60385
Aresidues: 1-629 < CAS>
Aresidues: 1-629 < CAS>
Aresidues: 1-629 < CAS>
Arecession: $60385
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Arecession: $6039
Arecession: $6030
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C;Keywords: transmembrane protein
F:50-66/Domain: transmembrane #status predicted <TMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;125-141/Domain: transmembrane #status predicted F;157-173/Domain; transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SGD:FRE7
A;Cross-references: SGD:S0005512; MIPS:YOL152w
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17; 123 GTFLVVMAJTLYTLLYCFVP---HPFYR-PCAGFGSPPLSV---RAGIMAISLVPFVFSL 175 326 RRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMGLGLLSLLAVTSIP---- 380 216 LRQARH---EGGYERMH----QRWKASDMWR-----SGVPPILFLNLLMLSSLPIARRH.262 214 GPVVVAISLATFFELYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLSLVY-L 272 273 AG-----LLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPM 325 381 --SVSNALNWREFSFIQSTLGYVALLISTFHV-----LIYGWKRAFEEEYYR- 425 263 FYEIFLQLHW-----ILAVGFYISLF---YHVYPELNSHMYLVATIVVW---FAQLFYRL 311 77; Indels 83; : Score 107.5; DE; Pred. No. 0.92; 46; Mismatches ----FYTPPNFVLALVLPSIVIL 444 312 AVKGYLRPGRSFMASTIANVSIV 334 Query Match
Best Local Similarity 21.7%;
Matches 57; Conservative 4 8 g ò 유 õ qq 장. ^업 ò

DB 2;

Search completed: March 14, 2001, 16:14:04 Job tlme: 105 sec

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